L5 ANSWER 1 OF 2 MEDLINE on STN

ACCESSION NUMBER: 2005066499 IN-PROCESS

DOCUMENT NUMBER: PubMed ID: 15536075

TITLE: A novel peptide isolated from a phage display peptide library with trastuzumab can mimic antigen epitope

of HER-2.

AUTHOR: Jiang Beihai; Liu Wenbin; Qu Hong; Meng Lin; Song Shumei;

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SOURCE: Journal of biological chemistry, (2005 Feb 11) 280 (6)

4656-62. Electronic Publication: 2004-11-09.

Journal code: 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: NONMEDLINE; IN-PROCESS; NONINDEXED; Priority Journals

OTHER SOURCE: PDB-1Y2N

ENTRY DATE: Entered STN: 20050208

Last Updated on STN: 20050301

AB Trastuzumab, a humanized antibody to HER-2, has been shown to be effective in the treatment of breast cancer in which HER-2 overexpression and metastasis occurs. In our search for an effective mimic epitope of HER-2 binding with trastuzumab and to develop HER-2 peptide vaccine, we screened a phage display 12-mer peptide library with trastuzumab as the target. A mimetic peptide (mimotope) H98 (LLGPYELWELSH) that could specifically recognize trastuzumab was isolated. The DNA encoding peptide H98 was cloned and expressed as the fusion protein GST-H98 in Escherichia coli BL21. The purified GST-H98 could specifically bind to trastuzumab and block the binding of trastuzumab to HER-2 protein. Moreover, H98 could significantly block the function of trastuzumab inhibiting the growth of cancer cells. Mice that were immunized with GST-H98 made specific antibody to H98 as well as to HER-2. In addition, T-cell proliferation occurred in mice immunized with GST-H98. Although no sequence homology was found between H98 and HER-2, through the use of structure analysis we were able to determine that peptide H98 contributed to a conformational epitope of HER-2. Furthermore, we determined that the last two amino acids at the C terminus, and the third together with the fourth amino acid at the N terminus of peptide H98 are critical to the binding of H98 to trastuzumab. As a result, we conclude that peptide H98 has potential for being developed as a HER-2 vaccine for biotherapy of cancer with HER-2 overexpression.

L5 ANSWER 2 OF 2 MEDLINE ON STN ACCESSION NUMBER: 2003239187 MEDLINE DOCUMENT NUMBER: PubMed ID: 12761188

TITLE: Molecular structural and functional characterization of

tumor suppressive anti-ErbB-2 monoclonal antibody by phage

display system.

AUTHOR: Itoh Kunihiko; Inoue Kazuyuki; Tezuka Takehiko; Tada

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SOURCE: Journal of biochemistry, (2003 Feb) 133 (2) 239-45.

Journal code: 0376600. ISSN: 0021-924X.

PUB. COUNTRY: Japan

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AB056117; GENBANK-AB056118

ENTRY MONTH: 200402

ENTRY DATE: Entered STN: 20030523

Last Updated on STN: 20040224 Entered Medline: 20040223

AB To investigate the molecular structural and functional characteristics of

tumor-suppressive anti-ErbB-2 monoclonal antibody (mAb) SER4, we performed mAb-gene cloning and epitope mapping by a phage display system. Structural analysis demonstrated that both the heavy chain (HC) and light chain variable regions are highly homologous with the derived germline sequences, while the HC complementarity determining region (HCDR) 3 has a relatively short length and biased amino acid usage. A cloned gene-derived recombinant Fab (rFab) fragment showed antigen binding activity and specificity comparable to the parent mAb. Cross-linking of the rFab fragment with the anti-Fab antibody elicited cell growth inhibition in vitro. These results imply that the cloned genes actually encode the Fab part of SER4. The epitope mimetic peptide (mimotope) isolated by panning a phage-displayed random peptide library against SER4 showed no cross-reactivity with mAbs other than SER4. The mimotope was found to be homologous with (87) AHNQVRQVPLQR (98) in the extracellular domain of ErbB-2 by means of a clustalw search. Since SER4 causes the growth inhibition of ErbB-2 positive cells, the predicted epitope sequence may constitute the putative functional domain of ErbB-2.

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